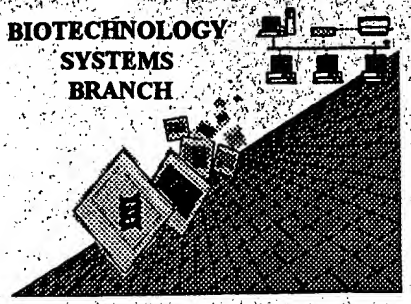
Revised

FILE COPY

BIOTECHNOLOGY SYSTEMS BRANCH

#B

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

RECEIVED
JUL 12 2000
TECH CENTER 1600/2900

Application Serial Number: 09/005,318B

Source: 1646

Date Processed by STIC: 6/23/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY**

or,

2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

D. Romeo

1646

RAW SEQUENCE LISTING DATE: 06/23/2000
PATENT APPLICATION: US/09/005,318B TIME: 06:20:30

Input Set : A:\401c1.app
Output Set: N:\CRF3\06222000\I005318B.raw

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

```
      4 (1) GENERAL INFORMATION:
C-->  6       (i) APPLICANT: Hein, Mich B.
      7                    Hiatt, Andrew C.
      8                    Fitchen, John H.
     10      (ii) TITLE OF INVENTION: NOVEL EPITHELIAL TISSUE TARGETING AGENT
     12     (iii) NUMBER OF SEQUENCES: 140
     14      (iv) CORRESPONDENCE ADDRESS:
     15           (A) ADDRESSEE: SEED IP LAW GROUP PLLC
     16           (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
     17           (C) CITY: Seattle
     18           (D) STATE: Washington
     19           (E) COUNTRY: USA
     20           (F) ZIP: 98104
     22       (v) COMPUTER READABLE FORM:
     23           (A) MEDIUM TYPE: Floppy disk
     24           (B) COMPUTER: IBM PC compatible
     25           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     26           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
C--> 28      (vi) CURRENT APPLICATION DATA:
C--> 29           (A) APPLICATION NUMBER: US/09/005,318B
C--> 30           (B) FILING DATE: 09-Jan-1998
     31           (C) CLASSIFICATION:
     33    (viii) ATTORNEY/AGENT INFORMATION:
     34           (A) NAME: Sharkey, Richard G.
     35           (B) REGISTRATION NUMBER: 32,629
     36           (C) REFERENCE/DOCKET NUMBER: 310098.401C1
     38      (ix) TELECOMMUNICATION INFORMATION:
     39           (A) TELEPHONE: (206) 622-4900
     40           (B) TELEFAX: (206) 682-6031
```

ERRORED SEQUENCES

```
E--> 472 (2) INFORMATION FOR SEQ ID NO:
     459       (i) SEQUENCE CHARACTERISTICS:
     475            (A) LENGTH: 286 base pairs
     476            (B) TYPE: nucleic acid
     477            (C) STRANDEDNESS: single
     478            (D) TOPOLOGY: linear
     467       (ix) FEATURE:
     468            (A) NAME/KEY: CDS
     469            (B) LOCATION: 1..282
     480       (ix) FEATURE:
     481            (A) NAME/KEY: CDS
     482            (B) LOCATION: 1..282
E--> 488       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
```

Delete duplicate material (see back page)

RAW SEQUENCE LISTING DATE: 06/23/2000
PATENT APPLICATION: US/09/005,318B TIME: 06:20:30

Input Set : A:\40lc1.app
Output Set: N:\CRF3\06222000\I005318B.raw

```
     490 GAT CAG AAG TGC AAG TGT GCT CGT ATT ACT TCT AGA ATC ATC CGT AGC        48
     491 Asp Gln Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser
W--> 492  15                  20                  25                  30
     494 TCA GAG GAC CCA AAT GAA GAT ATA GTC GAA CGT AAC ATC CGT ATC ATC        96
     495 Ser Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile
W--> 496                  35                  40                  45
     498 GTC CCA CTG AAT AAC CGG GAG AAT ATC TCA GAT CCT ACA AGT CCG TTG       144
     499 Val Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu
W--> 500              50                  55                  60
     502 CGC ACA CGC TTC GTA TAC CAC CTG TCA GAT CTG TGT AAG AAG TGT GAT       192
     503 Arg Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp
W--> 504          65                  70                  75
     506 CCA ACA GAG GTA GAG CTG GAC AAT CAG ATA GTC ACT GCG ACT CAA AGC       240
     507 Pro Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser
W--> 508       80                  85                  90
     510 AAC ATT TGC GAT GAG GAC AGC GCT ACA GAA ACC TGC TAC TGA               282
     511 Asn Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr
W--> 512  95                  100                 105
     514 ATTC                                                              286
E--> 517 (2) INFORMATION FOR SEQ ID NO: 14:
     519      (i) SEQUENCE CHARACTERISTICS:
     520           (A) LENGTH: 105 base pairs
     521           (B) TYPE: nucleic acid
     522           (C) STRANDEDNESS: single
     523           (D) TOPOLOGY: linear
     525     (ix) FEATURE:
     526           (A) NAME/KEY: CDS
     527           (B) LOCATION: 1..105
     533     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
     535 GAT CTG TGT AAG AAG TGT GAT CCA ACA GAG GTA GAG CTG GAC AAT CAG        48
     536 Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp Asn Gln
W--> 537  95                  100                 105                 110
     539 ATA GTC ACT GCG ACT CAA AGC AAC ATT TGC GAT GAG GAC AGC GCT ACA        96
     540 Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser Ala Thr
W--> 541                 115                 120                 125
     543 GAA ACC TGC                                                       105
     544 Glu Thr Cys
    1191 (2) INFORMATION FOR SEQ ID NO: 45:
    1193      (i) SEQUENCE CHARACTERISTICS:
    1194           (A) LENGTH: 16 amino acids
    1195           (B) TYPE: amino acid
    1196           (C) STRANDEDNESS:
    1197           (D) TOPOLOGY: linear
    1203     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
E--> 1205
     Ala Ile Gln Asp Pro Arg Leu Phe Ala Glu Glu Lys Ala Val Ala Asp
     1                5                  10                  15
    2303 (2) INFORMATION FOR SEQ ID NO: 111:
    2305      (i) SEQUENCE CHARACTERISTICS:
    2306           (A) LENGTH: 30 amino acids
    2307           (B) TYPE: amino acid
```


I insert hard return so that numbers will be under amino acids

RAW SEQUENCE LISTING DATE: 06/23/2000
PATENT APPLICATION: US/09/005,318B TIME: 06:20:31

Input Set : A:\401c1.app
Output Set: N:\CRF3\06222000\I005318B.raw

```
     2308          (C) STRANDEDNESS:
     2309          (D) TOPOLOGY: linear
     2314     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:
     2316   Val Arg Asp Gln Ala Gln Glu Asn Arg Ala Ser Gly Asp Ala Gly
E--> 2317       1               5       10      15
     2319   Ser Ala Asp Gly Gln Ser Arg Ser Ser Ser Ser Lys Val Leu Phe
E--> 2320   16      20   25      30
     2322 (2) INFORMATION FOR SEQ ID NO: 112:
     2324      (i) SEQUENCE CHARACTERISTICS:
     2325          (A) LENGTH: 25 amino acids
     2326          (B) TYPE: amino acid
     2327          (C) STRANDEDNESS:
     2328          (D) TOPOLOGY: linear
     2334     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:
     2336   Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr
E--> 2337       1               5                   10      15
     2339   Pro Ser Pro Ser Cys Cys His Pro Arg Leu
E--> 2340   16      20   25
```

← (misobjected amino acid nos)

fix nos

← (see item 4 on Error Summary Sheet)

VERIFICATION SUMMARY DATE: 06/23/2000
PATENT APPLICATION: US/09/005,318B TIME: 06:20:32

Input Set : A:\401cl.app
Output Set: N:\CRF3\06222000\I005318B.raw

L:6 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:28 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:433 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:480 M:201 W: Mandatory field data missing, SeqNo=13, [INFORMATION FOR SEQ ID NO:]
L:480 M:202 E: (16) Value must be an Integer, Data=[]
L:488 M:212 E: (34) Invalid or duplicate Sequence ID Number, Data=[13:]
L:492 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:-1
L:496 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:-1
L:500 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:-1
L:504 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:-1
L:508 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:-1
L:512 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:-1
L:517 M:216 E: (34) Seq.#s missing, 15 thru 13
L:537 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:541 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:42
L:1152 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:42
L:1205 M:203 E: No. of Seq. differs, LENGTH:Input:16 Found:0 SEQ:45
L:2317 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:111
M:332 Repeated in SeqNo=111
L:2337 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:112
M:332 Repeated in SeqNo=112
L:2486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118
L:2489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118
L:2640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:123
L:2646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:123
L:2649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:123

STATISTICS SUMMARY DATE: 06/23/2000
PATENT APPLICATION: US/09/005,318B TIME: 06:20:32

Input Set : A:\401c1.app
Output Set: N:\CRF3\06222000\I005318B.raw

Application Serial Number: US/09/005,318B
Alpha or Numeric: Alpha
Application Class: 514
Application File Date: 01-09-1998
Art Unit: 1646
Software Application: PatentIn
Total Number of Sequences: 140
Number of Errors: 8
Number of Warnings: 19
Number of Corrections: 4

MESSAGE SUMMARY

201 W: 1 (Mandatory field data missing)
202 E: 1 ((16) Value must be an Integer)
203 E: 1 (No. of Seq. differs)
212 E: 1 ((34) Invalid or duplicate Sequence ID Number)
216 E: 1 ((34) Seq.#s missing)
220 C: 4 (Keyword misspelled or invalid format)
332 E: 4 ((32) Invalid/Missing Amino Acid Numbering)
341 W: 7 ((46) "n" or "Xaa" used)
336 W: 11 (Invalid Amino Acid Number in Coding Region)